GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 14, 2006, 13:10:13 ; Search time 190 Seconds
(without alignments)
1271.886 Million cell updates/sec

Title: US-09-763-824B-37
Perfect score: 2836
Sequence: 1 MEDAKNIKKGPAPFYPLEDG.....DARKIREILIKAKKGGKSKL 550

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2836	100.0	550	2	AAR50011	Aar50011 Firefly l
2	2836	100.0	550	2	AAY08523	Aay08523 P. pyrali
3	2836	100.0	550	4	AAB31172	Aab31172 Amino aci
4	2836	100.0	550	6	ABU08537	Abu08537 American
5	2836	100.0	550	6	AAO27519	Aao27519 Firefly (
6	2836	100.0	550	8	ADO43720	Ado43720 Luciferas
7	2836	100.0	550	8	ADO24329	Ado24329 Photinus
8	2836	100.0	895	6	AAO27513	Aao27513 Hygromyci
9	2836	100.0	1242	5	ABB81108	Abb81108 LUC-U3'-U
10	2836	100.0	1242	6	ABB84637	Abb84637 LUC-U3'-U
11	2833	99.9	1172	7	ADJ14196	Adj14196 N-termina
12	2830	99.8	550	2	AAR83006	Aar83006 Firefly l
13	2830	99.8	550	2	AAR98515	Aar98515 P. pyrali

14	2830	99.8	1172	7	ADM18349	Adm18349 His6-BCCP
15	2829	99.8	743	2	AAR54867	Aar54867 Hepatitis
16	2829	99.8	743	2	AAR72801	Aar72801 Vaccinia
17	2828	99.7	550	2	AAR98518	Aar98518 P. pyrali
18	2828	99.7	550	2	AAW92747	Aaw92747 P. pyrali
19	2828	99.7	815	2	AAR28127	Aar28127 Lux::npt-
20	2826	99.6	550	9	ADZ27249	Adz27249 Wild type
21	2825	99.6	550	2	AAR86627	Aar86627 Firefly l
22	2821	99.5	550	5	AAU98564	Aau98564 Firefly l
23	2819	99.4	550	9	ADZ27245	Adz27245 Modified
24	2817	99.3	552	4	AAB35498	Aab35498 Synthetic
25	2812	99.2	550	2	AAW32936	Aaw32936 Modified
26	2812	99.2	550	4	AAB35055	Aab35055 Plant sig
27	2812	99.2	550	6	ABR43621	Abr43621 Cloning v
28	2812	99.2	550	7	ABR84631	Abr84631 Vector PB
29	2812	99.2	550	7	ABR84632	Abr84632 Vector PB
30	2812	99.2	550	8	ADR50836	Adr50836 Common ea
31	2812	99.2	550	8	ADS17727	Ads17727 Firefly l
32	2812	99.2	550	9	ADW70856	Adw70856 RNA inter
33	2812	99.2	550	9	ADW70854	Adw70854 RNA inter
34	2812	99.2	550	9	ADZ76988	Adz76988 Firefly l
35	2812	99.2	550	9	AEB68264	Aeb68264 Nuclear h
36	2812	99.2	550	9	AEB68272	Aeb68272 Nuclear h
37	2812	99.2	550	9	AEB68268	Aeb68268 Nuclear h
38	2812	99.2	805	8	ADS17729	Ads17729 Luciferas
39	2812	99.2	846	6	ABP58189	Abp58189 Luciferas
40	2812	99.2	893	6	ABP58187	Abp58187 Luciferas
41	2812	99.2	928	9	ADY71599	Ady71599 Human IRE
42	2812	99.2	975	5	ADI16793	Adi16793 NOVX prot
43	2812	99.2	2274	8	ADS17731	Ads17731 Luciferas
44	2810	99.1	550	9	ADZ27247	Adz27247 Modified
45	2804	98.9	550	6	ABU08534	Abu08534 American

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 14, 2006, 13:17:43 ; Search time 47 Seconds
(without alignments)
967.481 Million cell updates/sec

Title: US-09-763-824B-37
Perfect score: 2836
Sequence: 1 MEDAKNIKKGPAPFYPLEDG.....DARKIREILIKAKKGGKSKL 550

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2836	100.0	550	2	US-08-867-352-23	Sequence 23, Appl
2	2836	100.0	550	2	US-09-380-061B-21	Sequence 21, Appl
3	2836	100.0	550	2	US-09-602-628-12	Sequence 12, Appl
4	2836	100.0	550	2	US-09-396-154-31	Sequence 31, Appl
5	2836	100.0	550	2	US-09-980-585A-3	Sequence 3, Appli
6	2836	100.0	815	1	US-08-122-520C-9	Sequence 9, Appli
7	2836	100.0	1172	2	US-10-154-515A-4	Sequence 4, Appli
8	2836	100.0	1172	2	US-10-122-706-4	Sequence 4, Appli
9	2836	100.0	1242	2	US-09-488-270A-2	Sequence 2, Appli
10	2832	99.9	549	1	US-08-354-240A-2	Sequence 2, Appli
11	2830	99.8	550	2	US-08-718-425-2	Sequence 2, Appli
12	2830	99.8	550	2	US-08-875-277A-2	Sequence 2, Appli
13	2828	99.7	550	2	US-09-380-061B-6	Sequence 6, Appli
14	2825	99.6	550	2	US-08-718-425-5	Sequence 5, Appli
15	2823	99.5	550	2	US-08-875-277A-4	Sequence 4, Appli
16	2821	99.5	550	2	US-08-487-183A-10	Sequence 10, Appl

17	2812	99.2	550	1	US-08-354-240A-4	Sequence 4, Appli
18	2812	99.2	550	2	US-09-602-628-8	Sequence 8, Appli
19	2812	99.2	550	2	US-09-577-424-2	Sequence 2, Appli
20	2804	98.9	550	2	US-09-602-628-4	Sequence 4, Appli
21	2802	98.8	550	1	US-08-354-240A-6	Sequence 6, Appli
22	2792	98.4	550	2	US-09-602-628-2	Sequence 2, Appli
23	2779	98.0	561	1	US-08-474-169-8	Sequence 8, Appli
24	2766	97.5	550	2	US-09-602-628-6	Sequence 6, Appli
25	2428.5	85.6	547	2	US-09-380-061B-20	Sequence 20, Appl
26	2428.5	85.6	547	2	US-09-396-154-32	Sequence 32, Appl
27	2341.5	82.6	548	2	US-09-396-154-30	Sequence 30, Appl
28	2306.5	81.3	552	2	US-09-111-752-5	Sequence 5, Appli
29	2084.5	73.5	552	2	US-09-111-752-7	Sequence 7, Appli
30	2080.5	73.4	552	2	US-09-111-752-10	Sequence 10, Appl
31	2029	71.5	552	1	US-08-231-729B-6	Sequence 6, Appli
32	2029	71.5	552	2	US-09-396-154-33	Sequence 33, Appl
33	2029	71.5	666	2	US-09-581-894A-16	Sequence 16, Appl
34	2029	71.5	683	2	US-09-581-894A-14	Sequence 14, Appl
35	2029	71.5	684	2	US-09-581-894A-18	Sequence 18, Appl
36	2029	71.5	684	2	US-09-581-894A-20	Sequence 20, Appl
37	2029	71.5	715	2	US-09-581-894A-5	Sequence 5, Appli
38	1954.5	68.9	548	1	US-07-903-047-8	Sequence 8, Appli
39	1954.5	68.9	548	2	US-09-380-061B-16	Sequence 16, Appl
40	1954.5	68.9	548	2	US-08-487-183A-14	Sequence 14, Appl
41	1954.5	68.9	548	2	US-09-396-154-28	Sequence 28, Appl
42	1954.5	68.9	548	2	US-09-581-241A-8	Sequence 8, Appli
43	1951.5	68.8	548	1	US-07-675-211-2	Sequence 2, Appli
44	1951.5	68.8	548	1	US-07-903-047-2	Sequence 2, Appli
45	1951.5	68.8	548	1	US-08-076-042-2	Sequence 2, Appli

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 14, 2006, 13:18:28 ; Search time 169 Seconds
(without alignments)
1359.800 Million cell updates/sec

Title: US-09-763-824B-37
Perfect score: 2836
Sequence: 1 MEDAKNIKKGPAPFYPLEDG.....DARKIREILIKAKKGGKSKL 550

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2836	100.0	550	3	US-09-838-469-31	Sequence 31, Appl
2	2836	100.0	550	4	US-10-348-074-34	Sequence 34, Appl
3	2836	100.0	550	4	US-10-378-168-31	Sequence 31, Appl
4	2836	100.0	550	5	US-10-677-777-2	Sequence 2, Appli
5	2836	100.0	895	4	US-10-348-074-47	Sequence 47, Appl
6	2836	100.0	1172	4	US-10-122-706-4	Sequence 4, Appli
7	2836	100.0	1172	5	US-10-494-073-4	Sequence 4, Appli
8	2826	99.6	550	5	US-10-954-840-6	Sequence 6, Appli
9	2819	99.4	550	5	US-10-954-840-2	Sequence 2, Appli
10	2812	99.2	550	5	US-10-604-340-2	Sequence 2, Appli
11	2812	99.2	550	5	US-10-604-340-4	Sequence 4, Appli
12	2812	99.2	550	5	US-10-957-433-103	Sequence 103, App
13	2812	99.2	550	6	US-11-035-623-10	Sequence 10, Appl
14	2812	99.2	550	6	US-11-035-623-14	Sequence 14, Appl
15	2812	99.2	550	6	US-11-035-623-18	Sequence 18, Appl
16	2812	99.2	975	4	US-10-072-012-329	Sequence 329, App

17	2810	99.1	550	5	US-10-954-840-4	Sequence 4, Appli
18	2802	98.8	938	5	US-10-838-770-6	Sequence 6, Appli
19	2428.5	85.6	547	3	US-09-838-469-32	Sequence 32, Appl
20	2428.5	85.6	547	4	US-10-378-168-32	Sequence 32, Appl
21	2341.5	82.6	548	3	US-09-838-469-30	Sequence 30, Appl
22	2341.5	82.6	548	4	US-10-378-168-30	Sequence 30, Appl
23	2029	71.5	552	3	US-09-838-469-33	Sequence 33, Appl
24	2029	71.5	552	4	US-10-378-168-33	Sequence 33, Appl
25	1954.5	68.9	548	3	US-09-838-469-28	Sequence 28, Appl
26	1954.5	68.9	548	4	US-10-378-168-28	Sequence 28, Appl
27	1954.5	68.9	548	5	US-10-829-250-8	Sequence 8, Appli
28	1951.5	68.8	548	3	US-09-838-469-27	Sequence 27, Appl
29	1951.5	68.8	548	4	US-10-378-168-27	Sequence 27, Appl
30	1945.5	68.6	548	5	US-10-829-250-4	Sequence 4, Appli
31	1945.5	68.6	548	5	US-10-829-250-6	Sequence 6, Appli
32	1932	68.1	548	3	US-09-838-469-29	Sequence 29, Appl
33	1932	68.1	548	4	US-10-378-168-29	Sequence 29, Appl
34	1787	63.0	544	3	US-09-813-279B-3	Sequence 3, Appli
35	1787	63.0	544	4	US-10-378-168-44	Sequence 44, Appl
36	1787	63.0	544	4	US-10-655-878-3	Sequence 3, Appli
37	1787	63.0	544	5	US-10-895-596-3	Sequence 3, Appli
38	1784	62.9	544	5	US-10-746-995-3	Sequence 3, Appli
39	1778	62.7	544	3	US-09-838-469-24	Sequence 24, Appl
40	1778	62.7	544	3	US-09-813-279B-2	Sequence 2, Appli
41	1778	62.7	544	4	US-10-378-168-24	Sequence 24, Appl
42	1778	62.7	544	4	US-10-655-878-2	Sequence 2, Appli
43	1778	62.7	544	5	US-10-895-596-2	Sequence 2, Appli
44	1775	62.6	544	5	US-10-746-995-2	Sequence 2, Appli
45	1773	62.5	544	3	US-09-813-279B-4	Sequence 4, Appli

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 14, 2006, 13:19:23 ; Search time 22 Seconds
(without alignments)
695.872 Million cell updates/sec

Title: US-09-763-824B-37
Perfect score: 2836
Sequence: 1 MEDAKNIKKGPAPFYPLEDG.....DARKIREILIKAKKGGKSKL 550

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	797	28.1	542	7	US-11-087-099-1926	Sequence 1926, Ap
2	796.5	28.1	553	7	US-11-087-099-11332	Sequence 11332, A
3	793.5	28.0	547	7	US-11-087-099-4235	Sequence 4235, Ap
4	779.5	27.5	542	7	US-11-087-099-11825	Sequence 11825, A
5	772.5	27.2	545	7	US-11-087-099-8700	Sequence 8700, Ap
6	768.5	27.1	540	7	US-11-087-099-9739	Sequence 9739, Ap
7	766.5	27.0	545	7	US-11-087-099-2876	Sequence 2876, Ap
8	765.5	27.0	545	7	US-11-087-099-1574	Sequence 1574, Ap
9	756.5	26.7	543	7	US-11-087-099-1069	Sequence 1069, Ap
10	751.5	26.5	544	7	US-11-087-099-5596	Sequence 5596, Ap
11	748	26.4	550	7	US-11-096-568A-30775	Sequence 30775, A
12	704	24.8	441	7	US-11-096-568A-30776	Sequence 30776, A
13	680.5	24.0	550	7	US-11-096-568A-29167	Sequence 29167, A
14	680.5	24.0	550	7	US-11-096-568A-34190	Sequence 34190, A

15	659.5	23.3	371	7	US-11-096-568A-30777	Sequence 30777, A
16	658.5	23.2	479	7	US-11-096-568A-29168	Sequence 29168, A
17	658.5	23.2	479	7	US-11-096-568A-34191	Sequence 34191, A
18	644	22.7	530	7	US-11-096-568A-30779	Sequence 30779, A
19	638	22.5	440	7	US-11-096-568A-29169	Sequence 29169, A
20	638	22.5	440	7	US-11-096-568A-34192	Sequence 34192, A
21	590.5	20.8	421	7	US-11-096-568A-30780	Sequence 30780, A
22	567.5	20.0	349	7	US-11-096-568A-30781	Sequence 30781, A
23	557	19.6	578	7	US-11-087-099-1173	Sequence 1173, Ap
24	487	17.2	556	6	US-10-467-657-498	Sequence 498, App
25	470	16.6	236	7	US-11-087-099-10603	Sequence 10603, A
26	462	16.3	523	7	US-11-087-099-11876	Sequence 11876, A
27	420.5	14.8	401	6	US-10-510-386-68	Sequence 68, Appl
28	416	14.7	469	7	US-11-087-099-4058	Sequence 4058, Ap
29	416	14.7	715	7	US-11-087-099-808	Sequence 808, App
30	404.5	14.3	509	7	US-11-087-099-2985	Sequence 2985, Ap
31	397.5	14.0	578	7	US-11-087-099-2668	Sequence 2668, Ap
32	390	13.8	530	6	US-10-467-657-3804	Sequence 3804, Ap
33	387	13.6	469	7	US-11-087-099-719	Sequence 719, App
34	384	13.5	525	7	US-11-096-568A-24058	Sequence 24058, A
35	384	13.5	527	7	US-11-096-568A-24057	Sequence 24057, A
36	384	13.5	566	7	US-11-096-568A-24056	Sequence 24056, A
37	381.5	13.5	823	7	US-11-087-099-12259	Sequence 12259, A
38	379.5	13.4	552	7	US-11-087-099-1106	Sequence 1106, Ap
39	374	13.2	612	7	US-11-087-099-9710	Sequence 9710, Ap
40	373	13.2	553	7	US-11-087-099-1114	Sequence 1114, Ap
41	367.5	13.0	645	7	US-11-087-099-6116	Sequence 6116, Ap
42	362.5	12.8	484	7	US-11-087-099-8765	Sequence 8765, Ap
43	355.5	12.5	685	7	US-11-087-099-3131	Sequence 3131, Ap
44	354.5	12.5	683	7	US-11-087-099-2028	Sequence 2028, Ap
45	354	12.5	529	7	US-11-087-099-4223	Sequence 4223, Ap

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 14, 2006, 13:13:53 ; Search time 43 Seconds
(without alignments)
1230.680 Million cell updates/sec

Title: US-09-763-824B-37
Perfect score: 2836
Sequence: 1 MEDAKNIKKGPAPFYPLEDG.....DARKIREILIKAKKGGKSKL 550

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2836	100.0	550	1	A26772	Photinus-luciferin
2	2428.5	85.6	547	2	S62787	Photinus-luciferin
3	1954.5	68.9	548	1	S23437	Photinus-luciferin
4	1951.5	68.8	548	1	JS0181	Photinus-luciferin
5	1932	68.1	548	2	S33788	Photinus-luciferin
6	1347.5	47.5	543	2	S29354	Photinus-luciferin
7	1345.5	47.4	543	2	S29352	Photinus-luciferin
8	1342.5	47.3	543	2	S29355	Photinus-luciferin
9	1339.5	47.2	543	2	S29353	Photinus-luciferin
10	797	28.1	542	2	T03789	4-coumarate-CoA li
11	788.5	27.8	535	2	T08074	4-coumarate-CoA li
12	783	27.6	544	1	S01667	4-coumarate-CoA li
13	779.5	27.5	542	1	T02074	4-coumarate-CoA li
14	779	27.5	544	2	S15695	4-coumarate-CoA li
15	774	27.3	557	2	T07909	4-coumarate-CoA li
16	772.5	27.2	545	1	A39827	4-coumarate-CoA li
17	772.5	27.2	548	2	T07908	4-coumarate-CoA li
18	768.5	27.1	544	2	H85064	4-coumarate-CoA li

19	766.5	27.0	545	1	B39827	4-coumarate-CoA li
20	764	26.9	544	2	T20741	hypothetical prote
21	747	26.3	561	2	D96674	hypothetical prote
22	743	26.2	1549	2	D86338	protein F5M15.18 [
23	742	26.2	561	2	S57784	4-coumarate-CoA li
24	739.5	26.1	563	1	JU0311	4-coumarate-CoA li
25	730.5	25.8	570	2	T08075	4-coumarate-CoA li
26	722	25.5	542	2	B96654	hypothetical prote
27	715	25.2	537	2	T09755	4-coumarate-CoA li
28	714	25.2	537	2	T09710	4-coumarate-CoA li
29	702	24.8	569	2	T03390	4-coumarate-CoA li
30	672	23.7	566	2	F85214	4-coumarate-CoA li
31	672	23.7	566	2	T05038	4-coumarate-CoA li
32	669.5	23.6	423	2	PQ0772	4-coumarate-CoA li
33	619.5	21.8	293	2	S31705	4-coumarate-CoA li
34	611.5	21.6	552	2	E69438	probable fatty-aci
35	602.5	21.2	540	2	T18841	hypothetical prote
36	596	21.0	569	2	C69471	probable fatty-aci
37	591.5	20.9	566	2	H84037	long-chain fatty-a
38	573.5	20.2	564	2	G84037	long-chain fatty-a
39	568.5	20.0	566	2	T18607	hypothetical prote
40	567.5	20.0	565	2	D88197	protein ZK1127.2 [
41	549.5	19.4	593	2	E69378	probable acid-CoA
42	547.5	19.3	561	2	F85791	long-chain-fatty-a
43	547.5	19.3	561	2	B90943	long-chain-fatty-a
44	541.5	19.1	561	1	S41589	long-chain-fatty-a
45	540.5	19.1	548	2	D69187	probable acid-CoA

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 14, 2006, 13:10:38 ; Search time 224 Seconds
(without alignments)
1732.324 Million cell updates/sec

Title: US-09-763-824B-37
Perfect score: 2836
Sequence: 1 MEDAKNIKKGPAPFYPLEDG.....DARKIREILIKAKKGGKSKL 550

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2836	100.0	550	1	LUCI_PHOPY	P08659 photinus py
2	2832	99.9	550	2	Q27755_PHOPY	Q27755 photinus py
3	2812	99.2	832	2	Q75ZG1_9HEPC	Q75zg1 hepatitis c
4	2809	99.0	550	2	Q27758_PHOPY	Q27758 photinus py
5	2435.5	85.9	547	2	Q5UFR2_9COLE	Q5ufr2 lampyris tu
6	2428.5	85.6	547	2	Q27688_9COLE	Q27688 lampyris no
7	2398.5	84.6	547	2	Q5USC8_9COLE	Q5usc8 cratomorphu
8	2364.5	83.4	548	2	Q6SVE2_PYRRU	Q6sve2 pyrocoelia
9	2349.5	82.8	548	2	Q9GPF9_PYRRU	Q9gpf9 pyrocoelia
10	2341.5	82.6	548	2	Q26076_9COLE	Q26076 pyrocoelia
11	2336.5	82.4	548	2	Q6SVE1_PYRRU	Q6sve1 pyrocoelia
12	2270.5	80.1	527	2	Q6SVE0_9COLE	Q6sve0 lampyris no
13	2029	71.5	552	2	Q94697_PHOPE	Q94697 photuris pe
14	2023	71.3	552	2	Q94696_PHOPE	Q94696 photuris pe
15	1954.5	68.9	548	1	LUCI_LUCLA	Q01158 luciola lat
16	1954.5	68.9	548	2	Q27348_LUCLA	Q27348 luciola lat
17	1951.5	68.8	548	1	LUCI_LUCCR	P13129 luciola cru
18	1951.5	68.8	548	2	Q27321_LUCLA	Q27321 luciola lat
19	1950.5	68.8	548	2	Q8IRZ9_LUCLA	Q8irz9 luciola lat
20	1932	68.1	548	1	LUCI_LUCMI	Q26304 luciola min

21	1929	68.0	548	2	Q8T6U3_9COLE	Q8t6u3 hotaria unm
22	1925	67.9	548	2	Q8I0E8_9COLE	Q8i0e8 hotaria pap
23	1925	67.9	548	2	Q8ITG5_9COLE	Q8itg5 hotaria unm
24	1924	67.8	548	2	Q8ITG4_9COLE	Q8itg4 hotaria tsu
25	1921	67.7	548	2	Q25118_9COLE	Q25118 hotaria par
26	1917	67.6	548	2	Q8ITG3_9COLE	Q8itg3 hotaria tsu
27	1705.5	60.1	545	1	LUCI_PHOPE	Q27757 photuris pe
28	1584.5	55.9	545	2	Q9U4U8_9COLE	Q9u4u8 phrixothrix
29	1414	49.9	546	2	Q9U4U7_9COLE	Q9u4u7 phrixothrix
30	1354.5	47.8	543	2	Q718E3_9COLE	Q718e3 pyrophorus
31	1349.5	47.6	543	2	Q718C4_9COLE	Q718c4 pyrophorus
32	1349.5	47.6	543	2	Q718F0_9COLE	Q718f0 pyrophorus
33	1349.5	47.6	543	2	Q718F1_9COLE	Q718f1 pyrophorus
34	1348.5	47.5	543	2	Q718A7_9COLE	Q718a7 pyrophorus
35	1348.5	47.5	543	2	Q718D4_9COLE	Q718d4 pyrophorus
36	1347.5	47.5	543	2	Q7M4K2_9COLE	Q7m4k2 pyrophorus
37	1347.5	47.5	543	2	Q717B6_9COLE	Q717b6 pyrophorus
38	1347.5	47.5	543	2	Q718D7_9COLE	Q718d7 pyrophorus
39	1345.5	47.4	543	2	Q718E1_9COLE	Q718e1 pyrophorus
40	1345.5	47.4	543	2	Q7M4K3_9COLE	Q7m4k3 pyrophorus
41	1344.5	47.4	543	2	Q718D1_9COLE	Q718d1 pyrophorus
42	1344.5	47.4	543	2	Q718D3_9COLE	Q718d3 pyrophorus
43	1343.5	47.4	543	2	Q718C3_9COLE	Q718c3 pyrophorus
44	1343.5	47.4	543	2	Q718C5_9COLE	Q718c5 pyrophorus
45	1342.5	47.3	543	2	Q7M4K1_9COLE	Q7m4k1 pyrophorus